

## SEQUENCE LISTING

<110> Her Majesty the Queen in Right of Canada as Represented by the  
Minister of Agriculture and Agri-Food

<120> Regulation Of Gene Expression Using Chromatin Remodelling Factors

<130> 08-890985WO

<150> US 60/387,088

<151> 2002-06-06

<160> 104

<170> PatentIn version 3.0

<210> 1

<211> 142

<212> PRT

<213> WT-ROS

<400> 1

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Thr	Ala	Asp	Ile	Val	Ala	Ala	Tyr	Val	Ser	Asn	His	Val	Val	Pro	Val
			20					25					30		
Thr	Glu	Leu	Pro	Gly	Leu	Ile	Ser	Asp	Val	His	Thr	Ala	Leu	Ser	Gly
		35					40					45			
Thr	Ser	Ala	Pro	Ala	Ser	Val	Ala	Val	Asn	Val	Glu	Lys	Gln	Lys	Pro
	50					55					60				
Ala	Val	Ser	Val	Arg	Lys	Ser	Val	Gln	Asp	Asp	His	Ile	Val	Cys	Leu
65					70				75					80	
Glu	Cys	Gly	Gly	Ser	Phe	Lys	Ser	Leu	Lys	Arg	His	Leu	Thr	Thr	His
				85				90					95		
His	Ser	Met	Thr	Pro	Glu	Glu	Tyr	Arg	Glu	Lys	Trp	Asp	Leu	Pro	Val

100	105	110
Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu		
115	120	125
Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg		
130	135	140

&lt;210&gt; 2

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; synthetic ROS

&lt;400&gt; 2

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ttactgctga tatcggttgc gcttacgttt ctaaccacgt tggtcctggt actgagcttc      120
ctggacttat ctctgatggt catactgcac tttctggaac atctgctcct gcttctgttg      180
ctgttaacgt tgagaagcag aagcctgctg tttctgttcg taagtctggt caggatgata      240
atatcgtttg tttggagtgt ggtgggttctt tcaagtctct caagcgtcac cttactactc      300
atcactctat gactccagag gagtatagag agaagtggga tcttcctggt gattacccta      360
tggttgctcc tgcttacgct gaggctcggt ctcgtctcgc taaggagatg ggtctcggtc      420
agcgtcgtaa ggctaaccgt ccaaaaaaga agcgttaagg ctgagagctc gc              472

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&lt;210&gt; 3

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; consensus

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (447)

&lt;223&gt; where n is "a" or "c" or "t" or "g"

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (447)

<223> where d is "a" or "t" or "g"

<220>

<221> misc\_feature

<222> (1)..(447)

<223> where v is "a" or "c" or "g"

<220>

<221> misc\_feature

<222> (1)..(447)

<223> where k is "t" or "g"

<220>

<221> misc\_feature

<222> (1)..(447)

<223> where s is "c" or "g"

<220>

<221> misc\_feature

<222> (1)..(447)

<223> where w is "a" or "t"

<220>

<221> misc\_feature

<222> (1)..(447)

<223> where h is "a" or "t" or "c"

<220>

<221> misc\_feature

<222> (1)..(447)

<223> where b is "t" or "c" or "g"

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(447)

&lt;223&gt; where r is "a" or "g"

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(447)

&lt;223&gt; where y is "c" or "t"

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(447)

&lt;223&gt; where m is "a" or "c"

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gaygtncaya cngcnytnws nggnacnwsn gcncncngnw sngtngcngt naaygtngar	180
aarcaraarc cngcngtnws ngtnmgnaar wsngtncarg aygaycayat hgtntgyytn	240
gartgyggng gnwsnttyaa rwsnytnaar mgncayytna cnacncayca ywsnatgacn	300
ccngargart aymngararaa rtgggayytn ccngtngayt ayccnatggt ngcncncngn	360
taygcngarg cnmgwnsnmg nytngcnaar garatgggny tnggncarmg nmgnaaargcn	420
aaymgncna araaraarmg naargtn	447

&lt;210&gt; 4

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; synthetic ROS

&lt;400&gt; 4

Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu

[illegible]

<210> 5

<211> 10

<212> PRT

<213> ROS binding

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Trp Ala Thr Asp His Trp Lys Met Ala Arg  
1 . 5 10

<210> 6

<211> 7

<212> PRT

<213> NLS

<400> 6

Pro Lys Lys Lys Arg Lys Val  
1 5

<210>. 7

<211> 25

<212> DNA

<213> ROS operator

<400> 7  
tatatttcaa ttttattgta atata

25

<210> 8

<211> 27

<212> DNA

<213> IPT gene operator

<400> 8  
tataattaaa atattaactg tcgcatt

27

<210> 9

<211> 11

<212> DNA

<213> operator sequence binding to ERF

<400> 9  
taagagccgc c

11

<210> 10

<211> 9

<212> DNA

<213> operator sequence binding to SEBF

<400> 10  
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9

<210> 11

<211> 9

<212> DNA

<213> operator sequence binding to CBF

( <400> 11  
taccgacat

9

<210> 12

<211> 8

<212> DNA

<213> operator sequence binding to CBF

<400> 12  
tggccgac

8

<210> 13

<211> 16

<212> PRT

<213> NLS of AGAMOUS protein

<400> 13

Arg Ile Glu Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg  
1                      5                      10                      15

<210> 14

<211> 18

<212> PRT

<213> NLS of TGA-1A protein

<400> 14

Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg  
1                      5                      10                      15

Lys Lys

<210> 15

<211> 21

<212> PRT

<213> NLS of TGA-1B protein

<400> 15

Lys Lys Arg Ala Arg Leu Val Arg Asn Arg Glu Ser Ala Gln Leu Ser  
 1 5 10 15

Arg Gln Arg Lys Lys  
 20

<210> 16

<211> 18

<212> PRT

<213> NLS of O2 NLS B protein

<400> 16

Arg Lys Arg Lys Glu Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Tyr  
 1 5 10 15

Arg Lys

<210> 17

<211> 45

<212> PRT

<213> NLS of NIa protein

<220>

<221> LIPID

<222> (1)..(45)

<223> where "x" is any amino acid

<400> 17

Lys Lys Asn Gln Lys His Lys Leu Lys Met Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Arg Lys  
 35 40 45

<210> 18

<211> 16

<212> PRT

<213> NLS nucleoplasmin protein



&lt;400&gt; 18

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys  
1 5 10 15

&lt;210&gt; 19

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; NLS of NO38 protein

&lt;400&gt; 19

Lys Arg Ile Ala Pro Asp Ser Ala Ser Lys Val Pro Arg Lys Lys Thr  
1 5 10 15

Arg

&lt;210&gt; 20

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; NLS of N1/N2 protein

&lt;400&gt; 20

Lys Arg Lys Thr Glu Glu Glu Ser Pro Leu Lys Asp Lys Asp Ala Lys  
1 5 10 15

Lys

&lt;210&gt; 21

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; NLS of Glucocorticoid receptor

&lt;400&gt; 21

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys  
1 5 10 15

Lys

&lt;210&gt; 22

<211> 17

<212> PRT

<213> NLS of Glucocorticoid a receptor

<400> 22

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys  
1 5 10 15

Lys

<210> 23

<211> 17

<212> PRT

<213> NLS of Glucocorticoid b receptor

<400> 23

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys  
1 5 10 15

Lys

<210> 24

<211> 17

<212> PRT

<213> NLS of Progesterone receptor

<400> 24

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys  
1 5 10 15

Lys

<210> 25

<211> 17

<212> PRT

<213> NLS of Androgen receptor

&lt;400&gt; 25

Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys  
 1 5 10 15

Lys

&lt;210&gt; 26

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; NLS of p53 protein

&lt;400&gt; 26

Arg Arg Cys Phe Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg  
 1 5 10 15

Lys

&lt;210&gt; 27

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; VirC/VirD operator sequence

&lt;400&gt; 27

tatatttcaa ttttattgta atata

25

&lt;210&gt; 28

&lt;211&gt; 108

&lt;212&gt; DNA

&lt;213&gt; ROS-OPDS

&lt;400&gt; 28

atctccactg acgtaagggg tgacgcacaa tcccactatc cttcgcaaga cccttcctct 60

atataatata tttcaatttt attgtaatat aacacggggg actctaga 108

&lt;210&gt; 29

&lt;211&gt; 113

&lt;212&gt; DNA

&lt;213&gt; ROS-OPDA

<400> 29  
gatcctctag agtcccccggt gttatattac aataaaattg aaatatatta tatagaggaa 60  
gggtcttgcg aaggatagtg ggattgtgcg tcatccctta cgtcagtgga gat 113

&lt;210&gt; 30

&lt;211&gt; 107

&lt;212&gt; DNA

&lt;213&gt; ROS-OPUS

<400> 30  
atctccactg acgtaaggga tgacgcacaa tctatatttc aattttattg taatatacta 60  
tataaggaag ttcatttcat ttggagagaa cacgggggac tctagag 107

&lt;210&gt; 31

&lt;211&gt; 111

&lt;212&gt; DNA

&lt;213&gt; ROS-OPUA

<400> 31  
gatcctctag agtcccccggt gttctctcca aatgaaatga acttccttat atagtatatt 60  
acaataaaat tgaaatatag attgtgctgc atcccttacg tcagtggaga t 111

&lt;210&gt; 32

&lt;211&gt; 108

&lt;212&gt; DNA

&lt;213&gt; ROS-OPPS

<400> 32  
atctccactg acgtaaggga tgacgcacaa tctatatttc aattttattg taatatacta 60  
tataatatat ttcaatttta ttgtaatata acacggggga ctctagag 108

&lt;210&gt; 33

&lt;211&gt; 112

<212> DNA

<213> ROS-OPPA

<400> 33  
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<210> 34

<211> 59

<212> DNA

<213> ROS-OP1

<400> 34  
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<210> 35

<211> 57

<212> DNA

<213> ROS-OP2

<400> 35  
cgattatatt acaataaaaat tgaaatatag ctatattaca ataaaattga aatatag 57

<210> 36

<211> 36

<212> DNA

<213> tms2 promoter sense primer

<400> 36  
tgcggatgca taagcttgct gacattgcta gaaaag 36

<210> 37

<211> 26

<212> DNA

<213> tms2 promoter anti-sense primer

<400> 37  
cggggatcct ttcagggcca tttcag

26

<210> 38

<211> 24

<212> DNA

<213> actin2 promoter sense primer

<400> 38  
aagcttatgt atgcaagagt cagc

24

<210> 39

<211> 24

<212> DNA

<213> actin2 promoter anti-sense primer

<400> 39  
ttgactagta tcagcctcag ccat

24

<210> 40

<211> 138

<212> DNA

<213> EcoRV to ATG of GUS

<400> 40  
gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca agacccttcc  
tctatataat atatttcaat ttattgtaa tataacacgg gggactctag aggatccccg  
ggtggtcagt cccttatg

60

120

138

<210> 41

<211> 136

<212> DNA

<213> EcoRV to ATG of GUS

<400> 41

gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata 60  
 ctatataagg aagttcattt catttggaga gaacacgggg gactctagag gatccccggg 120  
 tggtcagtc cttatg 136

<210> 42

<211> 137

<212> DNA

<213> EcoRV to ATG of GUS

<400> 42  
 gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata 60  
 ctatataata tttttcaatt ttattgtaat ataacacggg ggactctaga ggatccccgg 120  
 gtggtcagtc cttatg 137

<210> 43

<211> 237

<212> DNA

<213> EcoRV to ATG of GUS

<400> 43  
 gatatctcca ctgacgtaag ggatgacgca caatcccaact atccttcgca agacccttcc 60  
 tctatataat atatttcaat tttattgtaa tataacacgg gggactctag aggatcctat 120  
 atttcaattt tattgtaata tagctatatt tcaattttat tgtaatataa tcgatttcga 180  
 acccggggta ccgaattcct cgagtctaga ggatccccgg gtggtcagtc cttatg 237

<210> 44

<211> 31

<212> DNA

<213> forward primer for HDA19 A. thaliana, pDBLeu-HDA19

<400> 44  
 gcgtcgacga tggatactgg cggcaattcg c 31

<210> 45

<211> 32

<212> DNA

<213> reverse primer for HDA19 *A. thaliana*, pDBLeu-HDA19

<400> 45

aggcggccgc ttatgtttta ggaggaaacg cc

32

<210> 46

<211> 31

<212> DNA

<213> forward primer for Gen5 *Arabidopsis*, GST-Gen5

<400> 46

gcgtcgacga tggactctca ctcttccac c

31

<210> 47

<211> 31

<212> DNA

<213> reverse primer for Gen5 *Arabidopsis*, GST-Gen5

<400> 47

gcgcggccgc ctattgagat ttagcaccag a

31

<210> 48

<211> 31

<212> DNA

<213> reverse primer for HDA19, GST-HDA19

<400> 48

gcgcggccgc ttatgtttta ggaggaaacg c

31

<210> 49

<211> 29

<212> DNA

<213> forward primer for bnKCP1, 1-80, 1-160 (generation of mutants)



<400> 49  
gcaagcttat ggcaggagga ggaccaact 29

<210> 50  
<211> 29  
<212> DNA  
<213> reverse primer for bnKCP1 1-160 (generation of mutants)

<400> 50  
cgctcgagct cctcctcattc attgtcttc 29

<210> 51  
<211> 29  
<212> DNA  
<213> reverse primer for bnKCP1 1-80 (generation of mutants)

<400> 51  
cgctcgagat gaacaggcaa aagaggcat 29

<210> 52  
<211> 29  
<212> DNA  
<213> reverse primer for bnKCP1 (generation of mutants)

<400> 52  
cgctcgagct catcttcttc ttcttcttc 29

<210> 53  
<211> 30  
<212> DNA  
<213> forward primer for bnKCP1, 1-80 and 1-160 (in vivo assay and transactivation assay)

<400> 53  
gcgtcgacga tggcaggagg aggaccaact 30

<210> 54

<211> 31

<212> DNA

<213> reverse primer for bnKCP1

<400> 54

gcgcggccgc ctcattcttct tcttcttcct c

31

<210> 55

<211> 31

<212> DNA

<213> reverse primer for bnKCP1

<400> 55

gcgcggccgc atgaacaggc aaaagaggca t

31

<210> 56

<211> 31

<212> DNA

<213> reverse primer for bnKCP1

<400> 56

gcgcggccgc ctctctctca tcattgtctt c

31

<210> 57

<211> 45

<212> DNA

<213> forward primer for bnKCP1G188

<400> 57

gatgttcttg cgaggagacc aggattcaag aacagagcat tgaag

45

<210> 58

<211> 45

<212> DNA

<213> reverse primer for bnKCP1G188

<400> 58  
cttcaatgct ctgttcttga atcctggtct cctcgcaaga acatc 45

<210> 59

<211> 30

<212> DNA

<213> forward primer for bnKCP1 81-215

<400> 59  
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<210> 60

<211> 29

<212> DNA

<213> forward primer for entire encoding region of bnKCP1

<400> 60  
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<210> 61

<211> 29

<212> DNA

<213> reverse primer for entire coding region of bnKCP1

<400> 61  
cggagctcct catcttcttc ttcttcttc 29

<210> 62

<211> 7

<212> PRT

<213> pat7 NLS (PLNKKRR)

<400> 62

Pro Leu Asn Lys Lys Arg Arg  
1 5

<210> 63

<213> aa seq of ROSR (ROS receptor)

<400> 63

Met	Thr	Asp	Met	Ala	Thr	Gly	Asn	Ala	Pro	Glu	Leu	Leu	Val	Glu	Leu
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Thr	Ala	Asp	Ile	Val	Ala	Ala	Tyr	Val	Ser	Asn	His	Val	Val	Pro	Val
		20						25					30		
Ser	Asp	Leu	Ala	Asn	Leu	Ile	Ser	Asp	Val	His	Ser	Ala	Leu	Ser	Asn
		35					40					45			
Thr	Ser	Val	Pro	Gln	Pro	Ala	Ala	Ala	Val	Val	Glu	Lys	Gln	Lys	Pro
	50					55					60				
Ala	Val	Ser	Val	Arg	Lys	Ser	Val	Gln	Asp	Glu	Gln	Ile	Thr	Cys	Leu
65					70					75					80
Glu	Cys	Gly	Gly	Asn	Phe	Lys	Ser	Leu	Lys	Arg	His	Leu	Met	Thr	His
				85					90					95	
His	Ser	Leu	Ser	Pro	Glu	Glu	Tyr	Arg	Glu	Lys	Trp	Asp	Leu	Pro	Thr
			100					105					110		
Asp	Tyr	Pro	Met	Val	Ala	Pro	Ala	Tyr	Ala	Glu	Ala	Arg	Ser	Arg	Leu
		115					120					125			
Ala	Lys	Glu	Met	Gly	Leu	Gly	Gln	Arg	Arg	Lys	Arg	Gly	Arg	Gly	
	130					135					140				

<213> aa seq of ROSAR (ROS receptor)

<400> 64

Met	Thr	Glu	Thr	Ala	Tyr	Gly	Asn	Ala	Gln	Asp	Leu	Leu	Val	Glu	Leu
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Thr	Ala	Asp	Ile	Val	Ala	Ala	Tyr	Val	Ser	Asn	His	Val	Val	Pro	Val
			20					25					30		
Thr	Glu	Leu	Pro	Gly	Leu	Ile	Ser	Asp	Val	His	Thr	Ala	Leu	Ser	Gly
		35					40					45			
Thr	Ser	Ala	Pro	Ala	Ser	Val	Ala	Val	Asn	Val	Glu	Lys	Gln	Lys	Pro
	50					55					60				
Ala	Val	Ser	Val	Arg	Lys	Ser	Val	Gln	Asp	Asp	His	Ile	Val	Cys	Leu

65				70				75				80			
Glu	Cys	Gly	Gly	Ser 85	Phe	Lys	Ser	Leu	Lys 90	Arg	His	Leu	Thr	Thr 95	His
His	Ser	Met	Thr 100	Pro	Glu	Glu	Tyr	Arg 105	Glu	Lys	Trp	Asp	Leu 110	Gln	Val
Asp	Tyr	Pro 115	Met	Val	Ala	Pro	Ala 120	Tyr	Ala	Glu	Ala	Arg 125	Ser	Arg	Leu
Ala	Lys 130	Glu	Met	Gly	Leu	Gly 135	Gln	Arg	Arg	Lys	Ala 140	Asn	Arg		

<210> 65

<211> 143

<212> PRT

<213> aa seq of MucR (ROS receptor)

<400> 65

Met Thr Glu Thr Ser Leu Gly Thr Ser Asn Glu Leu Leu Val Glu Leu  
1 5 10 15

Thr Ala Glu Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val  
20 25 30

Ala Glu Leu Pro Thr Leu Ile Ala Asp Val His Ser Ala Leu Asn Asn  
35 40 45

Thr Thr Ala Pro Ala Pro Val Val Val Pro Val Glu Lys Pro Lys Pro  
50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp Gln Ile Thr Cys Leu  
65 70 75 80

Glu Cys Gly Gly Thr Phe Lys Ser Leu Lys Arg His Leu Met Thr His  
85 90 95

His Asn Leu Ser Pro Glu Glu Tyr Arg Asp Lys Trp Asp Leu Pro Ala  
100 105 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu  
115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Arg Gly Lys  
130 135 140

<210> 66

<211> 10

<212> DNA

<213> VirC/VirD DNA binding site seq (1)

<400> 66  
tatatttcaa

10

<210> 67

<211> 10

<212> DNA

<213> VirC/VirD DNA binding site seq (2)

<400> 67  
tatattacaa

10

<210> 68

<211> 10

<212> DNA

<213> ipt DNA binding site seq (1)

<400> 68  
tataattaaa

10

<210> 69

<211> 10

<212> DNA

<213> ipt DNA binding site seq (2)

<400> 69  
aatgcgacag

10

<210> 70

<211> 10

<212> DNA

<213> consensus DNA binding site seq

<400> 70  
tatahttcaa

10

<210> 71

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; bnKCP aa seq

&lt;400&gt; 71

Met Ala Gly Gly Gly Pro Thr Phe Ser Ile Glu Leu Ser Ala Tyr Gly  
1 5 10 15

Ser Asp Leu Pro Thr Asp Lys Ala Ser Gly Asp Ile Pro Asn Glu Glu  
20 25 30

Gly Ser Gly Leu Ser Arg Val Gly Ser Gly Ile Trp Ser Gly Arg Thr  
35 40 45

Val Asp Tyr Ser Ser Glu Ser Ser Ser Ser Ile Gly Thr Pro Gly Asp  
50 55 60

Ser Glu Glu Glu Asp Glu Glu Ser Glu Glu Asp Asn Asp Glu Glu Glu  
65 70 75 80

Leu Gly Leu Ala Ser Leu Arg Ser Leu Glu Asp Ser Leu Pro Ser Lys  
85 90 95

Gly Leu Ser Ser His Tyr Lys Gly Lys Ser Lys Ser Phe Gly Asn Leu  
100 105 110

Gly Glu Ile Gly Ser Val Lys Glu Val Pro Lys Gln Glu Asn Pro Leu  
115 120 125

Asn Lys Lys Arg Arg Leu Gln Ile Tyr Asn Lys Leu Ala Arg Lys Ser  
130 135 140

Phe Tyr Ser Trp Gln Asn Pro Lys Ser Met Pro Leu Leu Pro Val His  
145 150 155 160

Glu Asp Asn Asp Asp Glu Glu Gly Asp Asp Gly Asp Leu Ser Asp Glu  
165 170 175

Glu Arg Gly Gly Asp Val Leu Ala Arg Arg Pro Ser Phe Lys Asn Arg  
180 185 190

Ala Leu Lys Ser Met Ser Cys Phe Ala Leu Ser Asp Leu Gln Glu Glu  
195 200 205

Glu Glu Glu Glu Glu Asp Glu  
210 215

&lt;210&gt; 72

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; atKCP aa seq

&lt;400&gt; 72

Met Glu Leu Met Ala Lys Pro Thr Phe Ser Ile Glu Val Ser Gln Tyr  
 1 5 10 15  
 Gly Thr Thr Asp Leu Pro Ala Thr Glu Lys Ala Ser Ser Ser Ser Ser  
 20 25 30  
 Ser Phe Glu Thr Thr Asn Glu Glu Gly Val Glu Glu Ser Gly Leu Ser  
 35 40 45  
 Arg Ile Trp Ser Gly Gln Thr Ala Asp Tyr Ser Ser Asp Ser Ser Ser  
 50 55 60  
 Ile Gly Thr Pro Gly Asp Ser Glu Glu Asp Glu Glu Glu Ser Glu Asn  
 65 70 75 80  
 Glu Asn Asp Asp Val Ser Ser Lys Glu Leu Gly Leu Arg Gly Leu Ala  
 85 90 95  
 Ser Met Ser Ser Leu Glu Asp Ser Leu Pro Ser Lys Arg Gly Leu Ser  
 100 105 110  
 Asn His Tyr Lys Gly Lys Ser Lys Ser Phe Gly Asn Leu Gly Glu Ile  
 115 120 125  
 Gly Ser Val Lys Glu Val Ala Lys Gln Glu Asn Pro Leu Asn Lys Arg  
 130 135 140  
 Arg Arg Leu Gln Ile Cys Asn Lys Leu Ala Arg Lys Ser Phe Tyr Ser  
 145 150 155 160  
 Trp Gln Asn Pro Lys Ser Met Pro Leu Leu Pro Val Asn Glu Asp Glu  
 165 170 175  
 Asp Asp Asp Asp Glu Asp Asp Asp Glu Glu Asp Leu Lys Ser Gly Phe  
 180 185 190  
 Asp Glu Asn Lys Ser Ser Ser Asp Glu Glu Gly Val Lys Lys Val Val  
 195 200 205  
 Val Arg Lys Gly Ser Phe Lys Asn Arg Ala Tyr Lys Ser Arg Ser Cys  
 210 215 220  
 Phe Ala Leu Ser Asp Leu Ile Glu Glu Glu Asp Asp Asp Asp Asp Gln  
 225 230 235 240

&lt;210&gt; 73

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; atKCL1 aa seq -

&lt;400&gt; 73

Met Glu Val Leu Val Gly Ser Thr Phe Arg Asp Arg Ser Ser Val Thr  
 1 5 10 15



Thr His Asp Gln Ala Val Pro Ala Ser Leu Ser Ser Arg Ile Gly Leu  
 20 25 30  
 Arg Arg Cys Gly Arg Ser Pro Pro Pro Glu Ser Ser Ser Ser Val Gly  
 35 40 45  
 Glu Thr Ser Glu Asn Glu Glu Asp Glu Asp Asp Ala Val Ser Ser Ser  
 50 55 60  
 Gln Gly Arg Trp Leu Asn Ser Phe Ser Ser Ser Leu Glu Asp Ser Leu  
 65 70 75 80  
 Pro Ile Lys Arg Gly Leu Ser Asn His Tyr Ile Gly Lys Ser Lys Ser  
 85 90 95  
 Phe Gly Asn Leu Met Glu Ala Ser Asn Thr Asn Asp Leu Val Lys Val  
 100 105 110  
 Glu Ser Pro Leu Asn Lys Arg Arg Arg Leu Leu Ile Ala Asn Lys Leu  
 115 120 125  
 Arg Arg Arg Ser Ser Leu Ser Ser Phe Ser Ile Tyr Thr Lys Ile Asn  
 130 135 140  
 Pro Asn Ser Met Pro Leu Leu Ala Leu Gln Glu Ser Asp Asn Glu Asp  
 145 150 155 160  
 His Lys Leu Asn Asp Asp Asp Asp Asp Asp Ser Ser Ser Asp Asp  
 165 170 175  
 Glu Thr Ser Lys Leu Lys Glu Lys Arg Met Lys Met Thr Asn His Arg  
 180 185 190  
 Asp Phe Met Val Pro Gln Thr Lys Ser Cys Phe Ser Leu Thr Ser Phe  
 195 200 205  
 Gln Asp Asp Asp Asp Arg  
 210

&lt;210&gt; 74

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; atKCL2 aa seq

&lt;400&gt; 74

Met Val Gly Ser Ser Phe Gly Ile Gly Met Ala Ala Tyr Val Arg Asp  
 1 5 10 15  
 His Arg Gly Val Ser Ala Gln Asp Lys Ala Val Gln Thr Ala Leu Phe  
 20 25 30  
 Leu Ala Asp Glu Ser Gly Arg Gly Gly Ser Gln Ile Gly Ile Gly Leu  
 35 40 45  
 Arg Met Ser Asn Asn Asn Asn Lys Ser Pro Glu Glu Ser Ser Asp Ser  
 50 55 60

Ser Ser Ser Ile Gly Glu Ser Ser Glu Asn Glu Glu Glu Glu Glu Glu  
 65 70 75 80  
 Asp Asp Ala Val Ser Cys Gln Arg Gly Thr Leu Asp Ser Phe Ser Ser  
 85 90 95  
 Ser Leu Glu Asp Ser Leu Pro Ile Lys Arg Gly Leu Ser Asn His Tyr  
 100 105 110  
 Val Gly Lys Ser Lys Ser Phe Gly Asn Leu Met Glu Ala Ala Ser Lys  
 115 120 125  
 Ala Lys Asp Leu Glu Lys Val Glu Asn Pro Phe Asn Lys Arg Arg Arg  
 130 135 140  
 Leu Val Ile Ala Asn Lys Leu Arg Arg Arg Gly Arg Ser Ile Thr Tyr  
 145 150 155 160  
 Glu Glu Asp His His Ile His Asn Asp Asp Tyr Glu Asp Asp Asp Gly  
 165 170 175  
 Asp Gly Asp Asp His Arg Lys Ile Met Met Met Met Lys Asn Lys Lys  
 180 185 190  
 Glu Leu Met Ala Gln Thr Arg Ser Cys Phe Cys Leu Ser Ser Leu Gln  
 195 200 205  
 Glu Glu Asp Asp Gly Asp Gly Asp Asp Asp Glu Asp Glu  
 210 215 220

&lt;210&gt; 75

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; bnKCP aa seq

&lt;400&gt; 75

Gly Asp Asp Gly Asp Leu Ser Asp Glu Glu Arg Gly Gly Asp Val Leu  
 1 5 10 15  
 Ala Arg Arg Pro Ser Phe Lys Asn Arg Ala Leu Lys Ser Met Ser Cys  
 20 25 30  
 Phe Ala Leu Ser Asp Leu Gln Glu Glu Glu  
 35 40

&lt;210&gt; 76

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; ATF-1 aa seq

&lt;400&gt; 76

Asp Ser Ser Asp Ser Ile Gly Ser Ser Gln Gln Ala His Gly Ile Leu  
 1 5 10 15

Ala Arg Arg Pro Ser Tyr Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu  
 20 25 30

Asp Thr Arg Gly Arg Lys Gly Asp Gly Glu  
 35 40

<210> 77

<211> 42

<212> PRT

<213> hyCREB aa seq

<400> 77

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu  
 1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp  
 20 25 30

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu  
 35 40

<210> 78

<211> 42

<212> PRT

<213> CREB aa seq

<400> 78

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu  
 1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp  
 20 25 30

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu  
 35 40

<210> 79

<211> 42

<212> PRT

<213> CREM aa seq

<400> 79

Ser Ala Asp Ser Glu Val Ile Asp Ser His Lys Arg Arg Glu Ile Leu  
1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Glu Leu Ser Ser Asp  
20 25 30

Val Pro Gly Ile Pro Lys Ile Glu Glu Glu  
35 40

<210> 80

<211> 42

<212> PRT

<213> cCREM aa seq.

<400> 80

Ala Glu Ser Glu Gly Val Ile Asp Ser His Lys Arg Arg Glu Ile Leu  
1 5 10 15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Glu Leu Ser Ser Asp  
20 25 30

Val Pro Gly Val Pro Lys Ile Glu Glu Glu  
35 40

<210> 81

<211> 461

<212> PRT

<213> aa seq of BNSCL1

<400> 81

Met Lys Leu Gln Ala Ser Ser Pro Gln Asp Asn Gln Pro Ser Asn Thr  
1 5 10 15

Thr Asn Asn Ser Thr Asp Ser Asn His Leu Ser Met Asp Glu His Ala  
20 25 30

Met Arg Ser Met Asp Trp Asp Ser Ile Met Lys Glu Leu Glu Val Asp  
35 40 45

Asp Asp Ser Ala Pro Tyr Gln Leu Gln Pro Ser Ser Phe Asn Leu Pro  
50 55 60

Val Phe Pro Asp Ile Asp Ser Ser Asp Val Tyr Pro Gly Pro Asn Gln  
65 70 75 80

Ile Thr Gly Tyr Gly Phe Asn Ser Leu Asp Ser Val Asp Asn Gly Gly  
85 90 95

Phe Asp Tyr Ile Glu Asp Leu Ile Arg Val Val Asp Cys Ile Glu Ser  
100 105 110

Asp Glu Leu His Leu Ala His Val Val Leu Ser Gln Leu Asn Gln Arg  
 115 120 125  
 Leu Gln Thr Ser Ala Gly Arg Pro Leu Gln Arg Ala Ala Phe Tyr Phe  
 130 135 140  
 Lys Glu Ala Leu Gly Ser Leu Leu Thr Gly Thr Asn Arg Asn Gln Leu  
 145 150 155 160  
 Phe Ser Trp Ser Asp Ile Val Gln Lys Ile Arg Ala Ile Lys Glu Phe  
 165 170 175  
 Ser Gly Ile Ser Pro Ile Pro Leu Phe Ser His Phe Thr Ala Asn Gln  
 180 185 190  
 Ala Ile Leu Asp Ser Leu Ser Ser Gln Ser Ser Ser Pro Phe Val His  
 195 200 205  
 Val Val Asp Phe Glu Ile Gly Phe Gly Gly Gln Tyr Ala Ser Leu Met  
 210 215 220  
 Arg Glu Ile Ala Glu Lys Ser Ala Asn Gly Gly Phe Leu Arg Val Thr  
 225 230 235 240  
 Ala Val Val Ala Glu Asp Cys Ala Val Glu Thr Arg Leu Val Lys Glu  
 245 250 255  
 Asn Leu Thr Gln Phe Ala Ala Glu Met Lys Ile Arg Phe Gln Ile Glu  
 260 265 270  
 Phe Val Leu Met Lys Thr Phe Glu Ile Leu Ser Phe Lys Ala Ile Arg  
 275 280 285  
 Phe Val Asp Gly Glu Arg Thr Val Val Leu Ile Ser Pro Ala Ile Phe  
 290 295 300  
 Arg Arg Val Ile Gly Ile Ala Glu Phe Val Asn Asn Leu Gly Arg Val  
 305 310 315 320  
 Ser Pro Asn Val Val Val Phe Val Asp Ser Glu Gly Cys Thr Glu Thr  
 325 330 335  
 Ala Gly Ser Gly Ser Phe Arg Arg Glu Phe Val Ser Ala Phe Glu Phe  
 340 345 350  
 Tyr Thr Met Val Leu Glu Ser Leu Asp Ala Ala Ala Pro Pro Gly Asp  
 355 360 365  
 Leu Val Lys Lys Ile Val Glu Thr Phe Leu Leu Arg Pro Lys Ile Ser  
 370 375 380  
 Ala Ala Val Glu Thr Ala Ala Asn Arg Arg Ser Ala Gly Gln Met Thr  
 385 390 395 400  
 Trp Arg Glu Met Leu Cys Ala Ala Gly Met Arg Pro Val Gln Leu Ser  
 405 410 415  
 Gln Phe Ala Asp Phe Gln Ala Glu Cys Leu Leu Glu Lys Ala Gln Val  
 420 425 430  
 Arg Gly Phe His Val Ala Lys Arg Gln Gly Glu Leu Val Leu Cys Trp  
 435 440 445

His Gly Arg Ala Leu Val Ala Thr Ser Ala Trp Arg Phe  
 450 455 460

<210> 82

<211> 486

<212> PRT

<213> aa seq of atSCL15

<400> 82

Met Lys Ile Pro Ala Ser Ser Pro Gln Asp Thr Thr Asn Asn Asn Asn  
 1 5 10 15

Asn Thr Asn Ser Thr Asp Ser Asn His Leu Ser Met Asp Glu His Val  
 20 25 30

Met Arg Ser Met Asp Trp Asp Ser Ile Met Lys Glu Leu Glu Leu Asp  
 35 40 45

Asp Asp Ser Ala Pro Asn Ser Leu Lys Thr Gly Phe Thr Thr Thr Thr  
 50 55 60

Thr Asp Ser Thr Ile Leu Pro Leu Tyr Ala Val Asp Ser Asn Leu Pro  
 65 70 75 80

Gly Phe Pro Asp Gln Ile Gln Pro Ser Asp Phe Glu Ser Ser Ser Asp  
 85 90 95

Val Tyr Pro Gly Gln Asn Gln Thr Thr Gly Tyr Gly Phe Asn Ser Leu  
 100 105 110

Asp Ser Val Asp Asn Gly Gly Phe Asp Phe Ile Glu Asp Leu Ile Arg  
 115 120 125

Val Val Asp Cys Val Glu Ser Asp Glu Leu Gln Leu Ala Gln Val Val  
 130 135 140

Leu Ser Arg Leu Asn Gln Arg Leu Arg Ser Pro Ala Gly Arg Pro Leu  
 145 150 155 160

Gln Arg Ala Ala Phe Tyr Phe Lys Glu Ala Leu Gly Ser Phe Leu Thr  
 165 170 175

Gly Ser Asn Arg Asn Pro Ile Arg Leu Ser Ser Trp Ser Glu Ile Val  
 180 185 190

Gln Arg Ile Arg Ala Ile Lys Glu Tyr Ser Gly Ile Ser Pro Ile Pro  
 195 200 205

Leu Phe Ser His Phe Thr Ala Asn Gln Ala Ile Leu Asp Ser Leu Ser  
 210 215 220

Ser Gln Ser Ser Ser Pro Phe Val His Val Val Asp Phe Glu Ile Gly  
 225 230 235 240

Phe Gly Gly Gln Tyr Ala Ser Leu Met Arg Glu Ile Thr Glu Lys Ser  
 245 250 255

Val Ser Gly Gly Phe Leu Arg Val Thr Ala Val Val Ala Glu Glu Cys  
 260 265 270  
 Ala Val Glu Thr Arg Leu Val Lys Glu Asn Leu Thr Gln Phe Ala Ala  
 275 280 285  
 Glu Met Lys Ile Arg Phe Gln Ile Glu Phe Val Leu Met Lys Thr Phe  
 290 295 300  
 Glu Met Leu Ser Phe Lys Ala Ile Arg Phe Val Glu Gly Glu Arg Thr  
 305 310 315 320  
 Val Val Leu Ile Ser Pro Ala Ile Phe Arg Arg Leu Ser Gly Ile Thr  
 325 330 335  
 Asp Phe Val Asn Asn Leu Arg Arg Val Ser Pro Lys Val Val Val Phe  
 340 345 350  
 Val Asp Ser Glu Gly Trp Thr Glu Ile Ala Gly Ser Gly Ser Phe Arg  
 355 360 365  
 Arg Glu Phe Val Ser Ala Leu Glu Phe Tyr Thr Met Val Leu Glu Ser  
 370 375 380  
 Leu Asp Ala Ala Ala Pro Pro Gly Asp Leu Val Lys Lys Ile Val Glu  
 385 390 395 400  
 Ala Phe Val Leu Arg Pro Lys Ile Ser Ala Ala Val Glu Thr Ala Ala  
 405 410 415  
 Asp Arg Arg His Thr Gly Glu Met Thr Trp Arg Glu Ala Phe Cys Ala  
 420 425 430  
 Ala Gly Met Arg Pro Ile Gln Gln Ser Gln Phe Ala Asp Phe Gln Ala  
 435 440 445  
 Glu Cys Leu Leu Glu Lys Ala Gln Val Arg Gly Phe His Val Ala Lys  
 450 455 460  
 Arg Gln Gly Glu Leu Val Leu Cys Trp His Gly Arg Ala Leu Val Ala  
 465 470 475 480  
 Thr Ser Ala Trp Arg Phe  
 485

&lt;210&gt; 83

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; aa seq lsSCR

&lt;400&gt; 83

Met Lys Val Pro Phe Ser Thr Asn Asp Asn Val Ser Ser Lys Pro Leu  
 1 5 10 15  
 Val Asn Ser Asn Asn Ser Phe Thr Phe Pro Ala Ala Thr Asn Gly Ser  
 20 25 30

Asn Leu Cys Tyr Glu Pro Lys Ser Val Leu Glu Leu Arg Arg Ser Pro  
 35 40 45  
 Ser Pro Ile Val Asp Lys Gln Ile Ile Thr Thr Asn Pro Asp Leu Ser  
 50 55 60  
 Ala Leu Cys Gly Gly Glu Asp Pro Leu Gln Leu Gly Asp His Val Leu  
 65 70 75 80  
 Ser Asn Phe Glu Asp Trp Asp Ser Leu Met Arg Glu Leu Gly Leu His  
 85 90 95  
 Asp Asp Ser Ala Ser Leu Ser Lys Thr Asn Pro Leu Thr His Ser Glu  
 100 105 110  
 Ser Leu Thr Gln Phe His Asn Leu Ser Glu Phe Ser Ala Glu Ser Asn  
 115 120 125  
 Gln Phe Pro Ser Pro Asp Phe Ser Phe Ser Asp Thr Asn Phe Pro Gln  
 130 135 140  
 Gln Phe Pro Thr Val Asn Gln Ala Ser Phe Ile Asn Ala Leu Asp Leu  
 145 150 155 160  
 Ser Gly Asp Ile His Gln Asn Trp Ser Val Gly Phe Asp Tyr Val Asp  
 165 170 175  
 Glu Leu Ile Arg Phe Ala Glu Cys Phe Glu Thr Asn Ala Phe Gln Leu  
 180 185 190  
 Ala His Val Ile Leu Ala Arg Leu Asn Gln Arg Leu Arg Ser Ala Ala  
 195 200 205  
 Gly Lys Pro Leu Gln Arg Ala Ala Phe Tyr Phe Lys Glu Ala Leu Gln  
 210 215 220  
 Ala Gln Leu Ala Gly Ser Ala Arg Gln Thr Arg Ser Ser Ser Ser Ser  
 225 230 235 240  
 Asp Val Ile Gln Thr Ile Lys Ser Tyr Lys Ile Leu Ser Asn Ile Ser  
 245 250 255  
 Pro Ile Pro Met Phe Ser Ser Phe Thr Ala Asn Gln Ala Val Leu Glu  
 260 265 270  
 Ala Val Asp Gly Ser Met Leu Val His Val Ile Asp Phe Asp Ile Gly  
 275 280 285  
 Leu Gly Gly His Trp Ala Ser Phe Met Lys Glu Leu Ala Asp Lys Ala  
 290 295 300  
 Glu Cys Arg Lys Ala Asn Ala Pro Ile Leu Arg Ile Thr Ala Leu Val  
 305 310 315 320  
 Pro Glu Glu Tyr Ala Val Glu Ser Arg Leu Ile Arg Glu Asn Leu Thr  
 325 330 335  
 Gln Phe Ala Arg Glu Leu Asn Ile Gly Phe Glu Ile Asp Phe Val Leu  
 340 345 350  
 Ile Arg Thr Phe Glu Leu Leu Ser Phe Lys Ala Ile Lys Phe Met Glu  
 355 360 365



Gly Glu Lys Thr Ala Val Leu Leu Ser Pro Ala Ile Phe Arg Arg Val  
 370 375 380  
 Gly Ser Gly Phe Val Asn Glu Leu Arg Arg Ile Ser Pro Asn Val Val  
 385 390 395 400  
 Val His Val Asp Ser Glu Gly Leu Met Gly Tyr Gly Ala Met Ser Phe  
 405 410 415  
 Arg Gln Thr Val Ile Asp Gly Leu Glu Phe Tyr Ser Thr Leu Leu Glu  
 420 425 430  
 Ser Leu Glu Ala Ala Asn Ile Gly Gly Gly Asn Cys Gly Asp Trp Met  
 435 440 445  
 Arg Lys Ile Glu Asn Phe Val Leu Phe Pro Lys Ile Val Asp Met Ile  
 450 455 460  
 Gly Ala Val Gly Arg Arg Gly Gly Gly Gly Ser Trp Arg Asp Ala Met  
 465 470 475 480  
 Val Asp Ala Gly Phe Arg Pro Val Gly Leu Ser Gln Phe Ala Asp Phe  
 485 490 495  
 Gln Ala Asp Cys Leu Leu Gly Arg Val Gln Val Arg Gly Phe His Val  
 500 505 510  
 Ala Lys Arg Gln Ala Glu Met Leu Leu Cys Trp His Asp Arg Ala Leu  
 515 520 525  
 Val Ala Thr Ser Ala Trp Arg Cys  
 530 535

&lt;210&gt; 84

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; BnSCL1 sense primer

&lt;400&gt; 84

gatggacgaa catgccatgc gttcca

26

&lt;210&gt; 85

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; BnSCL1 anti-sense primer

&lt;400&gt; 85

cgctcggatc ttctgaacaa t

21

&lt;210&gt; 86

<211> 21  
<212> DNA  
<213> BnIAA1 sense primer

<400> 86  
ccacgcgtcc ggtacgatga t 21

<210> 87  
<211> 22  
<212> DNA  
<213> BnIAA1 anti-sense primer

<400> 87  
gaagttgaga aatggtttat ga 22

<210> 88  
<211> 21  
<212> DNA  
<213> BnIAA12 sense primer

<400> 88  
acgctggtgc ttctcctcct c 21

<210> 89  
<211> 24  
<212> DNA  
<213> BNIAA12 anti-sense primer

<400> 89  
aaaacccatt agaagaacca agaa 24

<210> 90  
<211> 33  
<212> DNA  
<213> forward primer for BnSCL1, BnSCL1 1-358, BnSCL1 1-261, BnSCL1 1-217  
and BnSCL1 1-145 for pET-28b vector

<400> 90  
gcaagcttat ggacgaacat gccatgcgtt cca 33

<210> 91

<211> 29

<212> DNA

<213> reverse primer for BnSCL1 for pET-28b vector

<400> 91  
cgctcgagaa agcgccacgc tgacgtggc 29

<210> 92

<211> 29

<212> DNA

<213> reverse primer for BnSCL1 1-358 for pET-28b vector

<400> 92  
cgctcgagcg cggagatctt cggacgtaa 29

<210> 93

<211> 29

<212> DNA

<213> reverse primer for BnSCL1 1-261 for pET-28b vector

<400> 93  
cgctcgagcc taatcgctt gaaagataa 29

<210> 94

<211> 29

<212> DNA

<213> reverse primer for BnSCL1 1-217 for pET-28b vector

<400> 94  
cgctcgagcg ccacaaccgc cgtgactct 29

<210> 95

<211> 29

<212> DNA

<213> reverse primer for BnSCL1 1-145 for pET-28b vector

<400> 95

cgctcgagcg ctcggatctt ctgaacaat

29

<210> 96

<211> 34

<212> DNA

<213> forward primer for BnSCL1, BnSCL1 1-358, BnSCL1 1-261, BnSCL1 1-217 and BnSCL1 1-145 for PC86 vector

<400> 96

gcgtcgacga tggacgaaca tgccatgcgt tcca

34

<210> 97

<211> 30

<212> DNA

<213> forward primer for BnSCL1 146-358 for PC86 vector

<400> 97

gcgtcgacga ttaaggagtt ttccggtata

30

<210> 98

<211> 30

<212> DNA

<213> forward primer for BnSCL1 218-434 for PC86 vector

<400> 98

gcgtcgacgg aggattgcgc cgtcgagacg

30

<210> 99

<211> 31

<212> DNA

<213> reverse primer for BnSCL1 and BnSCL1 218-434 for PC86 vector

<400> 99  
gcgcggccgc aaagcgccac gctgacgtgg c 31

<210> 100

<211> 31

<212> DNA

<213> reverse primer for BnSCL1 1-358 for PC86 vector

<400> 100  
gcgcggccgc cgcgagatc ttcggacgta a 31

<210> 101

<211> 31

<212> DNA

<213> reverse primer for BnSCL1 1-261 for PC86 vector

<400> 101  
gcgcggccgc cctaatacgcc ttgaaagata a 31

<210> 102

<211> 31

<212> DNA

<213> reverse primer for BnSCL1 1-217 for PC86 vector

<400> 102  
gcgcggccgc cgccacaacc gccgtgactc t 31

<210> 103

<211> 31

<212> DNA

<213> reverse primer of BnSCL1 1-145 for PC86 vector

<400> 103  
gcgcggccgc cgctcggatc ttctgaacaa t 31

<210> 104

<211> 5

<212> PRT

<213> aa seq of LXXLL motif (148LGSL152)

<400> 104

Leu Gly Ser Leu Leu  
1 5